



SEQUENCE LISTING

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SEP 16 2003
TECH CENTER 1600/2900

<110> BOYLE, WILLIAM

<120> OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS

<130> A-451K REV 09-10-03 54SEQ

<140> US 09/721,212

<141> 2000-11-21

<150> US 09/052,521

<151> 1998-03-30

<150> US 08/880,855

<151> 1997-06-23

<150> US 08/842,842

<151> 1997-04-16

<160> 54

<170> PatentIn version 3.1

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1 5
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Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
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Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
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Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
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Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr
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Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp
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Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
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155 160 165
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Leu Thr Ile Asp Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr

aga tta att gaa gga gaa tta att tta att tta att tta att tta att
Thr Ile Ser Asp Gly Lys Ile Ala Val Asn Ile Arg Gly Phe Tyr Tyr

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 Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn
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 Lys Val Gln Asp Ile Asp
 315

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<213> Mus musculus

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130 135 140

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145 150

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210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
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260 265 270

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275 280 285

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<213> Homo sapiens

2001

 $\langle 221 \rangle$ COS $\langle 222 \rangle \quad (185) \dots (1135)$

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Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp	
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Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
50 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
65 70 75 80

Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
85 90 95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
100 105 110

Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
130 135 140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
145 150 155 160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
180 185 190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
210 215 220

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
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25 30 35	
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Arg His Tyr Glu His Leu Gly Arg Cys Cys Ser Arg Cys Glu Pro Gly	
40 45 50	
gag tac ctg tcc tct aag tgc act cct acc tcc gac agt gtg tgt ctg	245
Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr Ser Asp Ser Val Cys Leu	
55 60 65 70	

Sequence data from GenBank accession number U00001.1 (Escherichia coli K12 genome).

Sequence data from GenBank accession number U00001.1 (Escherichia coli K12 genome).

Asp	Pro	Gly	Asn	His	Thr	Ala	Pro	Arg	Arg	Cys	Ala	Cys	Thr	Ala	Gly		
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Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	Gly	Lys	Ala	Leu	Thr	Ala	Asn		
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Leu	Trp	Asn	Trp	Val	Asn	Asp	Ala	Cys	Ser	Ser	Leu	Ser	Gly	Asn	Lys		
		250						255					260				
gag	tcg	tca	ggg	gac	cgt	tgt	gct	ggg	tcg	cac	tgc	gca	acc	tcc	agt	869	
Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser	His	Ser	Ala	Thr	Ser	Ser		
		265				270						275					
cag	caa	gaa	gtg	tgt	gaa	ggt	atc	tta	cta	atg	act	ccc	cag	tac	aac	911	
Gln	Gln	Gln	Val	Cys	Gln	Gly	Ile	Leu	Leu	Met	Thr	Arg	Gln	Ile	Lys		
280					285					290							
atg	gtt	cca	gaa	gac	ggt	gct	gga	gtc	tgt	ggg	ccc	gtg	tct	tcc	gca	965	
Met	Val	Pro	Glu	Asp	Gly	Ala	Gly	Val	Cys	Gly	Pro	Val	Cys	Ala	Ala		
295					300				305					310			
ggt	ggg	ccc	tgg	gca	gaa	gtc	aca	gat	tct	agg	acg	ttc	aca	ctg	gtc	1013	
Gly	Gly	Pro	Trp	Ala	Gln	Val	Arg	Asp	Ser	Arg	Thr	Phe	Thr	Leu	Val		
				315					320					325			

Leu	Ile	Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro	Pro	Phe	Gln	Glu	Pro	Leu		
360						365					370						
gaa gtg ggg gag aac gac agt tta agc cag tgt ttc acc ggg act gaa 1205																	
Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	Cys	Phe	Thr	Gly	Thr	Glu		
375					380					385					390		
agc acg gtg gat tct gag ggc tgt gac ttc act gag cct ccg agc aga 1253																	
Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe	Thr	Glu	Pro	Pro	Ser	Arg		
				395					400					405			
act gac tct atg ccc gtg tcc cct gaa aag cac ctg aca aaa gaa ata 1301																	
Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys	His	Leu	Thr	Lys	Glu	Ile		
			410					415					420				
gaa ggt gac agt tgc ctc ccc tgg gtg gtc agc tcc aac tca aca gat 1349																	
Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val	Ser	Ser	Asn	Ser	Thr	Asp		
		425					430					435					
ggc tac aca ggc agt ggg aac act cct ggg gag gac cat gaa ccc ttt 1397																	
Gly	Tyr	Thr	Gly	Ser	Gly	Asn	Thr	Pro	Gly	Glu	Asp	His	Glu	Pro	Phe		
		440				445					450						
cca ggg tcc ctg aaa tgt gga cca ttg ccc cag tgt gcc tac agc atg 1445																	
Pro	Gly	Ser	Leu	Lys	Cys	Gly	Pro	Leu	Pro	Gln	Cys	Ala	Tyr	Ser	Met		
					460					465					470		
ggc ttt ccc agt gaa gca gca gcc agc atg gca gag gcg gga gta cgg 1493																	
Gly	Phe	Pro	Ser	Glu	Ala	Ala	Ala	Ser	Met	Ala	Glu	Ala	Gly	Val	Arg		
				475					480					485			
ccc cag gac agg gct gat gag agg gga gcc tca ggg tcc ggg agc tcc 1541																	
Pro	Gln	Asp	Arg	Ala	Asp	Glu	Arg	Gly	Ala	Ser	Gly	Ser	Gly	Ser	Ser		
				490				495					500				
ccc agt gac cag cca cct gcc tct ggg aac gtg act gga aac agt aac 1589																	
Pro	Ser	Asp	Gln	Pro	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	Ser	Asn		
		505					510					515					
tcc acg ttc atc tct agc ggg cag gtg atg aac ttc aag ggt gac atc 1637																	
Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	Asp	Ile		
		520				525					530						
atc gtg gtg tat gtc agc cag acc tcc cag gag ggc ccg ggt tcc gca 1685																	
Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Pro	Gly	Ser	Ala		
					540					545					550		
gag ccc gag tcc gag ccc gtg ggc cgc cct gtg cag gag gag acc ctg 1733																	
Glu	Pro	Glu	Ser	Glu	Pro	Val	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu		
				555					560					565			
gca cac aga gac tcc ttt gcg ggc acc gcg ccg cgc ttc ccc gac gtc 1781																	
Ala	His	Arg	Asp	Ser	Phe	Ala	Gly	Thr	Ala	Pro	Arg	Phe	Pro	Asp	Val		
			570					575						580			

Leu His Thr Gln Gly Ser Gly Gln Cys Ala Glu
615 620 625

gacctgggtg cagggcacca gtgcctttcc aaaaacatgg ttagctagc cactgtgcac 1990
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Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
35 40 45

Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
50 55 60

Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr
65 70 75 80

Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Tyr
85 90 95

Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
100 105 110

Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys

Arg Leu Asn Lys Arg Thr Val Tyr Thr Leu Tyr Thr Leu Tyr Thr Thr

Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys
165 170 175

Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp
180 185 190

Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala
195 200 205

Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val
210 215 220

Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly
225 230 235 240

Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser
245 250 255

Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser
260 265 270

His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu
275 280 285

Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys
290 295 300

Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser
305 310 315 320

Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser
325 330 335

Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro
340 345 350

Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro
355 360 365

Pro Phe Gln Gln Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln

Thr Leu Thr Thr Ser Ala Ile Asp Ser Met Leu Thr Ser Ile Thr Tyr

His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val
420 425 430

Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly
435 440 445

Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro
450 455 460

Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met
465 470 475 480

Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala
485 490 495

Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn
500 505 510

Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met
515 520 525

Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln
530 535 540

Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro
545 550 555 560

Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala
565 570 575

Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Gln Gln
580 585 590

Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Gln Gln
595 600 605

Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala
610 615 620

Gln

11111

11111 111

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Met His Leu Thr Ile Gln Asp Ile Asp
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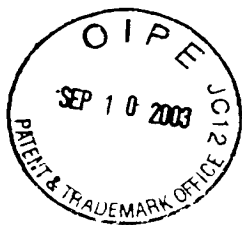
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Met

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- 29 -

<210> 54

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Lys Leu Val Thr Leu Gln Val Thr Pro
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